RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/774,221B_

Source: _1FW/6,_

Date Processed by STIC: _5/25/06_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 05/25/2006
PATENT APPLICATION: US/10/774,721B   TIME: 08:48:36

Input Set : A:\10-774721Sequence Listing.rev.5-18-06.txt
Output Set: N:\CRF4\05252006\J774721B.raw

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 3 <110> APPLICANT: JOCKERS, Ralf
 4        COUTURIER, Cyril
 5        UHLMANN, Eugen
 7 <120> TITLE OF INVENTION: OB RGRP
 9 <130> FILE REFERENCE: FRAV2003/0005 US NP
11 <140> CURRENT APPLICATION NUMBER: 10/774,721B
12 <141> CURRENT FILING DATE: 2004-02-09
14 <150> PRIOR APPLICATION NUMBER: 60/461,005
15 <151> PRIOR FILING DATE: 2003-04-07
17 <150> PRIOR APPLICATION NUMBER: 0301543
18 <151> PRIOR FILING DATE: 2003-02-10
20 <160> NUMBER OF SEQ ID NOS: 51
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 648
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
30 cactttattc tgattacagt gcattgaatt tcttagaact catactatct gtatacatgt      60
32 gcacatgcgg cattttacta tgaaatttaa tatgctgggt tttttaatac ctttatatat     120
34 catgttcact ttaagaaaga cttcataagt aggagatgag ttttattctc agcaaataga     180
36 cctgtcaaat ttagattatg ttactcaaat tatgttactt gtttggctgt tcatgtagtc     240
38 acggtgctct cagaaaatat attaacgcag tcttgtaggc agctgccacc ttatgcagtg     300
40 catcgaaacc ttttgcttgg ggatgtgctt ggagaggcag ataacgctga agcaggcctc     360
42 tcatgaccca ggaaggccgg ggtggatccc tctttgtgtt gtagtccatg ctattaaaag     420
44 tgtggcccac agaccaagag cctcaacatt tcctagagcc ttattagaaa tgcagaatct     480
46 gaagccccac tctggaccca ggacattttg atgagatcca aaggagttgt atgcacatga     540
48 aagtttgaga agcatcatca tagagaagta aacatcacac ccaacttcct tatctttcca     600
50 gtggctaaac cacttaacct ctctgggtgt acctgctca tttgttta                    648
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 20
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: AS14
61 <220> FEATURE:
62 <221> NAME/KEY: misc_feature
63 <223> OTHER INFORMATION: antisens AS14
66 <400> SEQUENCE: 2
67 aatgccgcat gtgcacatgt                                                   20
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 396
72 <212> TYPE: DNA
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 73 <213> ORGANISM: Homo sapiens
 75 <220> FEATURE:
 76 <221> NAME/KEY: CDS
 77 <222> LOCATION: (1)..(396)
 80 <400> SEQUENCE: 3
 81 atg gcg ggc gtt aaa gct ctc gtg gca tta tcc ttc agt ggg gct att      48
 82 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
 83 1               5                   10                  15
 85 gga ctg act ttt ctt atg ctg gga tgt gcc tta gag gat tat ggc gtt      96
 86 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
 87             20                  25                  30
 89 tac tgg ccc tta ttc gtc ctg att ttc cac gcc atc tcc ccc atc ccc     144
 90 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
 91         35                  40                  45
 93 cat ttc att gcc aaa aga gtc acc tat gac tca gat gca acc agt agt     192
 94 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
 95     50                  55                  60
 97 gcc tgt cgg gaa ctg gca tat ttc ttc act act gga att gtt gtt tct     240
 98 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
 99 65                  70                  75                  80
101 gcc ttt gga ttt cct gtt att ctt gct cgt gtg gct gtg atc aaa tgg     288
102 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
103             85                  90                  95
105 gga gcc tgc ggc ctt gtg ttg gca ggc aat gca gtc att ttc ctt aca     336
106 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
107             100                 105                 110
109 att caa ggg ttt ttc ctt ata ttt gga aga gga gat gat ttt agc tgg     384
110 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
111         115                 120                 125
113 gag cag tgg tag                                                     396
114 Glu Gln Trp
115     130
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 131
120 <212> TYPE: PRT
121 <213> ORGANISM: Homo sapiens
123 <400> SEQUENCE: 4
125 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
126 1               5                   10                  15
129 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
130             20                  25                  30
133 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
134         35                  40                  45
137 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
138     50                  55                  60
141 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
142 65                  70                  75                  80
145 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
146             85                  90                  95
```

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```
149 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
150             100             105             110
153 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
154         115             120             125
157 Glu Gln Trp
158     130
161 <210> SEQ ID NO: 5
162 <211> LENGTH: 1359
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: OB RGRP LUC
169 <220> FEATURE:
170 <221> NAME/KEY: misc_feature
171 <223> OTHER INFORMATION: OB RGRP LUC
174 <220> FEATURE:
175 <221> NAME/KEY: CDS
176 <222> LOCATION: (1)..(1359)
179 <400> SEQUENCE: 5
180 atg gcg ggc gtt aaa gct ctc gtg gca tta tcc ttc agt ggg gct att        48
181 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
182 1               5               10              15
184 gga ctg act ttt ctt atg ctg gga tgt gcc tta gag gat tat ggc gtt        96
185 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
186             20              25              30
188 tac tgg ccc tta ttc gtc ctg att ttc cac gcc atc tcc ccc atc ccc       144
189 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
190         35              40              45
192 cat ttc att gcc aaa aga gtc acc tat gac tca gat gca acc agt agt       192
193 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
194     50              55              60
196 gcc tgt cgg gaa ctg gca tat ttc ttc act act gga att gtt gtt tct       240
197 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
198 65              70              75              80
200 gcc ttt gga ttt cct gtt att ctt gct cgt gtg gct gtg atc aaa tgg       288
201 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
202             85              90              95
204 gga gcc tgc ggc ctt gtg ttg gca ggc aat gca gtc att ttc ctt aca       336
205 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
206             100             105             110
208 att caa ggg ttt ttc ctt ata ttt gga aga gga gat gat ttt agc tgg       384
209 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
210         115             120             125
212 gag cag tgg att ccg ggg gat cca ccg gct aga gcc acc atg acc agc       432
213 Glu Gln Trp Ile Pro Gly Asp Pro Pro Ala Arg Ala Thr Met Thr Ser
214     130             135             140
216 aag gtg tac gac ccc gag cag agg aag agg atg atc acc ggc ccc cag       480
217 Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln
218 145             150             155             160
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Input Set : A:\10-774721Sequence Listing.rev.5-18-06.txt
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220 tgg tgg gcc agg tgc aag cag atg aac gtg ctg gac agc ttc atc aac     528
221 Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn
222             165                 170                 175
224 tac tac gac agc gag aag cac gcc gag aac gcc gtg atc ttc ctg cac     576
225 Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His
226             180                 185                 190
228 ggc aac gcc gct agc agc tac ctg tgg agg cac gtg gtg ccc cac atc     624
229 Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile
230             195                 200                 205
232 gag ccc gtg gcc agg tgc atc atc ccc gat ctg atc ggc atg ggc aag     672
233 Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys
234         210                 215                 220
236 agc ggc aag agc ggc aac ggc agc tac agg ctg ctg gac cac tac aag     720
237 Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys
238 225                 230                 235                 240
240 tac ctg acc gcc tgg ttc gag ctc ctg aac ctg ccc aag aag atc atc     768
241 Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile Ile
242             245                 250                 255
244 ttc gtg ggc cac gac tgg ggc gcc tgc ctg gcc ttc cac tac agc tac     816
245 Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr Ser Tyr
246             260                 265                 270
248 gag cac cag gac aag atc aag gcc atc gtg cac gcc gag agc gtg gtg     864
249 Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser Val Val
250             275                 280                 285
252 gac gtg atc gag agc tgg gac gag tgg cca gac atc gag gag gac atc     912
253 Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile
254         290                 295                 300
256 gcc ctg atc aag agc gag gag ggc gag aag atg gtg ctg gag aac aac     960
257 Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn
258 305                 310                 315                 320
260 ttc ttc gtg gag acc atg ctg ccc agc aag atc atg aga aag ctg gag     1008
261 Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu
262             325                 330                 335
264 ccc gag gag ttc gcc gcc tac ctg gag ccc ttc aag gag aag ggc gag     1056
265 Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu
266             340                 345                 350
268 gtg aga aga ccc acc ctg agc tgg ccc aga gag atc ccc ctg gtg aag     1104
269 Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys
270             355                 360                 365
272 ggc ggc aag ccc gac gtg gtg cag atc gtg aga aac tac aac gcc tac     1152
273 Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr Asn Ala Tyr
274         370                 375                 380
276 ctg aga gcc agc gac gac ctg ccc aag atg ttc atc gag agc gac ccc     1200
277 Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro
278 385                 390                 395                 400
280 ggc ttc ttc agc aac gcc atc gtg gag ggc gcc aag aag ttc ccc aac     1248
281 Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn
282             405                 410                 415
284 acc gag ttc gtg aag gtg aag ggc ctg cac ttc agc cag gag gac gcc     1296
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285 Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala
286             420             425             430
288 ccc gac gag atg ggc aag tac atc aag agc ttc gtg gag aga gtg ctg      1344
289 Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val Leu
290         435             440             445
292 aag aac gag cag taa                                                  1359
293 Lys Asn Glu Gln
294     450
297 <210> SEQ ID NO: 6
298 <211> LENGTH: 452
299 <212> TYPE: PRT
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: OB RGRP LUC
305 <220> FEATURE:
306 <221> NAME/KEY: misc_feature
307 <223> OTHER INFORMATION: OB RGRP LUC
309 <400> SEQUENCE: 6
311 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
312 1           5               10              15
315 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
316         20              25              30
319 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
320         35              40              45
323 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
324     50              55              60
327 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
328 65              70              75              80
331 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
332             85              90              95
335 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
336         100             105             110
339 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
340         115             120             125
343 Glu Gln Trp Ile Pro Gly Asp Pro Pro Ala Arg Ala Thr Met Thr Ser
344     130             135             140
347 Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln
348 145             150             155             160
351 Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn
352             165             170             175
355 Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His
356         180             185             190
359 Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile
360         195             200             205
363 Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys
364     210             215             220
367 Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys
368 225             230             235             240
371 Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile Ile
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/25/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:51; Xaa Pos. 11,12,13,14,18,24,28,44,47,54,55,58,64,65,75,76,87,91,103
Seq#:51; Xaa Pos. 106,108,110,112,115,120,127,128,134,142,143,150

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:51

VERIFICATION SUMMARY DATE: 05/25/2006
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Output Set: **N:\CRF4\05252006\J774721B.raw**

L:3648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
M:341 Repeated in SeqNo=51